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results of BLAST

BLASTN 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1005939809-15110-323

Query=

(40 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).;
1,020,477 sequences; 4,355,661,355 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 54 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

		Score (bits)	E Value
gi 7706766 ref NM_016113.1	Homo sapiens vanilloid receptor...	66	1e-09
gi 5305597 gb AF103906.1 AF103906	Homo sapiens vanilloid re...	66	1e-09
gi 10184146 emb AX023795.1 AX023795	Sequence 1 from Patent ...	66	1e-09
gi 7023447 dbj AK001896.1 AK001896	Homo sapiens cDNA FLJ110...	58	4e-07
gi 15281201 gb AC010608.7	Homo sapiens chromosome 5 clone ...	38	0.33
gi 15451689 gb AC025464.5	Homo sapiens chromosome 5 clone ...	38	0.33
gi 6651379 gb AF172277.1 AF172277	Homo sapiens 7q21 clones ...	38	0.33
gi 11120966 gb AC007567.2 AC007567	Homo sapiens BAC clone C...	38	0.33
gi 15807672	Unknown	36	1.3
gi 15638817 gb AC080073.6	Homo sapiens chromosome 7 clone ...	36	1.3
gi 6460468 gb AE001862.1 AE001862	Deinococcus radiodurans R...	36	1.3
gi 5042401 gb AC007786.1 AC007786	Homo sapiens chromosome 1...	36	1.3
gi 6689159 emb AL136058.1 SCE20	Streptomyces coelicolor cos...	36	1.3
gi 3253129 gb AC004223.1 AC004223	Homo sapiens chromosome 1...	36	1.3
gi 298270 gb S55307.1 S55307	ATP nucleotide 3'-pyrophosphok...	36	1.3
gi 13470324	Unknown	34	5.2
gi 15805042	Unknown	34	5.2
gi 15144462 gb AC012500.7	Homo sapiens BAC clone RP11-434M...	34	5.2
gi 16596540 gb AC092365.3	Homo sapiens chromosome 16 clone...	34	5.2
gi 16195215 gb AC022103.5	Homo sapiens chromosome 5 clone ...	34	5.2
gi 15451661 gb AC010458.6	Homo sapiens chromosome 19 clone...	34	5.2
gi 13096815 gb BC003201.1 BC003201	Mus musculus, chondroiti...	34	5.2
gi 14150415 gb AC012476.8 AC012476	Homo sapiens chromosome ...	34	5.2
gi 10946955 ref NM_021528.1	Mus musculus chondroitin 4-sul...	34	5.2
gi 2588621 gb AC003084.1 AC003084	Human BAC clone CTB-84D4 ...	34	5.2
gi 3417290 gb U95737.1 HUU95737	Human Chromosome 16 BAC clo...	34	5.2
gi 4809180 gb AF136344.1 AF136344	Toxoplasma gondii catalas...	34	5.2
gi 3900858 gb AC004848.1 AC004848	Homo sapiens PAC clone RP...	34	5.2
gi 6458057 gb AE001898.1 AE001898	Deinococcus radiodurans R...	34	5.2
gi 15881473 emb AJ337055.1 HSA337055	Homo sapiens genomic s...	34	5.2
gi 15880290 emb AJ335872.1 HSA335872	Homo sapiens genomic s...	34	5.2
gi 15878939 emb AJ334521.1 HSA334521	Homo sapiens genomic s...	34	5.2
gi 15870433 emb AJ326039.1 HSA326039	Homo sapiens genomic s...	34	5.2
gi 5579391 gb AF161267.1 AF161267	Toxoplasma gondii catalas...	34	5.2
gi 14715658 emb AL161651.13 AL161651	Human DNA sequence fro...	34	5.2
gi 14041741 emb AL133351.33 AL133351	Human DNA sequence fro...	34	5.2
gi 10178502 emb AL355392.7 AL355392	Human DNA sequence from...	34	5.2
gi 13445335 emb AL161779.32 AL161779	Human DNA sequence fro...	34	5.2
gi 10944277 emb AL121753.30 HSDJ61404	Human DNA sequence fr...	34	5.2
gi 13274200 emb AL122008.28 HSJ799P18	Human DNA sequence fr...	34	5.2
gi 9408716 emb AL121980.14 HS1007G16	Human DNA sequence fro...	34	5.2
gi 3366580 gb AC004049.1 AC004049	Homo sapiens chromosome 4...	34	5.2
gi 7228177 emb AL133215.16 AL133215	Human DNA sequence from...	34	5.2
gi 57236 emb X16362.1 RNSERPG	Rat SPI-2 serine protease inh...	34	5.2
gi 8017427 emb AJ289132.1 MMU289132	Mus musculus mRNA for c...	34	5.2
gi 5420383 emb AL034384.1 HSMTM0	Human chromosome Xq28, cos...	34	5.2
gi 1698996 gb U78190.1 HSU78190	Human GTP cyclohydrolase I ...	34	5.2
gi 16549752 dbj AK055096.1 AK055096	Homo sapiens cDNA FLJ30...	34	5.2
gi 14588673 dbj AP003492.2 AP003492	Oryza sativa genomic DN...	34	5.2
gi 14023393 dbj AP003001.2 AP003001	Mesorhizobium loti DNA,...	34	5.2
gi 205037 gb M67496.1 RATKBP	Rat kallikrein-binding protein...	34	5.2
gi 13488765 dbj AP000802.4 AP000802	Homo sapiens genomic DN...	34	5.2
gi 13429916 dbj AP001922.4 AP001922	Homo sapiens genomic DN...	34	5.2
gi 12381920 dbj AP002815.3 AP002815	Homo sapiens genomic DN...	34	5.2

Alignments

>gi|7706766|ref|NM_016113.1| Homo sapiens vanilloid receptor-like protein (VRL), mRNA

Length = 2507

Score = 65.9 bits (33), Expect = 1e-09
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||||||||||||||||||||||||||||||
Sbjct: 77 ccgacgcgcagctgggaggaagacaggaccctt 109

>gi|5305597|gb|AF103906.1|AF103906 Homo sapiens vanilloid receptor-like protein (VRL
cds
Length = 2507

Score = 65.9 bits (33), Expect = 1e-09
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||||||||||||||||||||||
Sbjct: 77 ccgacgcgcagctgggaggaagacaggaccctt 109

>gi|10184146|emb|AX023795.1|AX023795 Sequence 1 from Patent WO0022121
Length = 2765

Score = 65.9 bits (33), Expect = 1e-09
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||||||||||||||||||
Sbjct: 269 ccgacgcgcagctgggaggaagacaggaccctt 301

>gi|7023447|dbj|AK001896.1|AK001896 Homo sapiens cDNA FLJ11034 fis, clone PLACE10042
Length = 2126

Score = 58.0 bits (29), Expect = 4e-07
Identities = 32/33 (96%)
Strand = Plus / Plus

Query: 8 ccgacgcgcagctgggaggaagacaggaccctt 40
|||||||||||||||||||||
Sbjct: 241 ccgacgcgcagctgggaggaagacaggccctt 273

>gi|15281201|gb|AC010608.7| Homo sapiens chromosome 5 clone CTB-3M24, complete seque
Length = 210408

Score = 38.2 bits (19), Expect = 0.33
Identities = 19/19 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagacag 33
|||||||||||||||||
Sbjct: 97477 gcagctgggaggaagacag 97495

>gi|15451689|gb|AC025464.5| Homo sapiens chromosome 5 clone CTD-2260C5, complete seq
Length = 115265

Score = 38.2 bits (19), Expect = 0.33
Identities = 19/19 (100%)

Strand = Plus / Minus

Query: 15 gcagctgggaggaagacag 33

|||||||||||||||||||

Sbjct: 81325 gcagctgggaggaagacag 81307

>gi|6651379|gb|AF172277.1|AF172277 Homo sapiens 7q21 clones 267017 and 256L2 includi
genes, complete sequence
Length = 227054

Score = 38.2 bits (19), Expect = 0.33

Identities = 19/19 (100%)

Strand = Plus / Plus

Query: 15 gcagctgggaggaagacag 33

|||||||||||||||||||

Sbjct: 40139 gcagctgggaggaagacag 40157

>gi|11120966|gb|AC007567.2|AC007567 Homo sapiens BAC clone CTB-36G2 from 7q31, compl
Length = 187413

Score = 38.2 bits (19), Expect = 0.33

Identities = 19/19 (100%)

Strand = Plus / Minus

Query: 15 gcagctgggaggaagacag 33

|||||||||||||||||||

Sbjct: 43518 gcagctgggaggaagacag 43500

Score = 36.2 bits (18), Expect = 1.3

Identities = 0/18 (0%)

Strand = Plus / Minus

Query: 2 acgaggccgacgcgcagc 19

>gi|15638817|gb|AC080073.6| Homo sapiens chromosome 7 clone RP11-321C7, complete seq
Length = 57075

Score = 36.2 bits (18), Expect = 1.3

Identities = 18/18 (100%)

Strand = Plus / Plus

Query: 17 agctgggaggaagacagg 34

|||||||||||||||||||

Sbjct: 36773 agctgggaggaagacagg 36790

>gi|6460468|gb|AE001862.1|AE001862 Deinococcus radiodurans R1 section 1 of 2 of the
Length = 213732

Score = 36.2 bits (18), Expect = 1.3

Identities = 18/18 (100%)

Strand = Plus / Minus

Query: 2 acgaggccgacgcgcagc 19

|||||||||||||||||||

Sbjct: 208524 acgaggccgacgcgcagc 208507

>gi|5042401|gb|AC007786.1|AC007786 Homo sapiens chromosome 19, BAC 41855 (CIT-B-32o4

Length = 229061

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 20 tgggaggaagacaggacc 37
|||
Sbjct: 175566 tqggaaqqaagacaqqacc 175583

>gi|6689159|emb|AL136058.1|SCE20 Streptomyces coelicolor cosmid E20
Length = 33820

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 2 acgaggccgcacgcgcagc 19
|||||||||||||||||||
Sbjct: 18706 acgaggccgcacgcgcagc 18689

>gi|3253129|gb|AC004223.1|AC004223 Homo sapiens chromosome 17, clone HRPC837J1, comp
Length = 101328

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 21 gggaggaagacaggaccc 38
| | | | | | | | | | | | | | | |
Sbjct: 78669 gggaggaagacaggaccc 78652

>gi|298270|gb|S55307.1|S55307 ATP nucleotide 3'-pyrophosphokinase [Streptomyces moro
Genomic, 1116 nt]
Length = 1116

Score = 36.2 bits (18), Expect = 1.3
Identities = 21/22 (95%)
Strand = Plus / Minus

```
Query: 1      cacgaggccgacgcgcagctgg 22
          ||||||| ||||| ||||||| ||||| |
Sbjct: 1110 cacgaggccatcgcccgagctgg 1089
```

Score = 34.2 bits (17), Expect = 5.2
Identities = 0/17 (0%)
Strand = Plus / Minus

Query: 3 cqaqqccqacqcqcqac 19

Score = 34.2 bits (17), Expect = 5.2
Identities = 0/17 (0%)
Strand = Plus / Minus

Query: 2 acgaaqqccqacqcqcaq 18

>gi|15144462|gb|AC012500.7| Homo sapiens BAC clone RP11-434M17 from 2, complete sequ

Length = 117763

Score = 34.2 bits (17), Expect = 5.2
Identities = 23/25 (92%)
Strand = Plus / Minus

Query: 15 gcagctgggaggaagacaggaccct 39
||||||| ||||| ||||| |||||
Sbjct: 111985 gcagctgggaggcagacagtaccct 111961

>gi|16596540|gb|AC092365.3| Homo sapiens chromosome 16 clone RP11-450B4, complete se
Length = 181329

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 19 ctgggaggaagacagga 35
||||||| ||||| |||||
Sbjct: 14707 ctgggaggaagacagga 14691

>gi|16195215|gb|AC022103.5| Homo sapiens chromosome 5 clone CTC-254B4, complete sequ
Length = 129175

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 17 agctgggaggaagacag 33
||||||| |||||
Sbjct: 123247 agctgggaggaagacag 123263

>gi|15451661|gb|AC010458.6| Homo sapiens chromosome 19 clone CTD-2265M8, complete se
Length = 105788

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 16 cagctgggaggaagaca 32
||||||| |||||
Sbjct: 98762 cagctgggaggaagaca 98746

>gi|13096815|gb|BC003201.1|BC003201 Mus musculus, chondroitin 4-sulfotransferase 2,
IMAGE:3586766, mRNA, complete cds
Length = 1785

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagac 31
||||||| |||||
Sbjct: 1284 gcagctgggaggaagac 1300

>gi|14150415|gb|AC012476.8|AC012476 Homo sapiens chromosome 15 clone RP11-532F12 map
sequence
Length = 178248

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 9 cgacgcgcagctgggag 25
 |||||||||||||||||||
Sbjct: 77450 cgacgcgcagctgggag 77434

>gi|10946955|ref|NM_021528.1| Mus musculus chondroitin 4-sulfotransferase 2 (C4st2-p
Length = 1715

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagac 31
 |||||||||||||||||||
Sbjct: 1216 gcagctgggaggaagac 1232

>gi|2588621|gb|AC003084.1|AC003084 Human BAC clone CTB-84D4 from 7q31, complete sequ
Length = 166219

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 21 gggaggaagacaggacc 37
 |||||||||||||||||||
Sbjct: 150301 gggaggaagacaggacc 150285

>gi|3417290|gb|U95737.1|HUU95737 Human Chromosome 16 BAC clone CIT987SK-A-388D4, com
 sapiens]
Length = 93431

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 19 ctgggaggaagacagga 35
 |||||||||||||||||||
Sbjct: 17754 ctgggaggaagacagga 17770

>gi|4809180|gb|AF136344.1|AF136344 Toxoplasma gondii catalase mRNA, complete cds
Length = 2448

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 24 aggaagacaggaccctt 40
 |||||||||||||||||||
Sbjct: 1730 aggaagacaggaccctt 1746

>gi|3900858|gb|AC004848.1|AC004848 Homo sapiens PAC clone RP4-649P17 from 7q11.23-q2
Length = 135214

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 24 aggaagacaggaccctt 40

|||||||||||||||||

Sbjct: 104601 aggaagacaggaccctt 104617

>gi|6458057|gb|AE001898.1|AE001898 Deinococcus radiodurans R1 section 35 of 229 of t
chromosome 1
Length = 12523

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Minus

Query: 2 acgaggccgacgcgcag 18

|||||||||||||||||

Sbjct: 6963 acgaggccgacgcgcag 6947

>gi|15881473|emb|AJ337055.1|HSA337055 Homo sapiens genomic sequence surrounding NotI
Length = 780

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Plus

Query: 21 gggaggaagacaggacc 37

|||||||||||||||||

Sbjct: 657 gggaggaagacaggacc 673

>gi|15880290|emb|AJ335872.1|HSA335872 Homo sapiens genomic sequence surrounding NotI
Length = 731

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34

|||||||||||||||||

Sbjct: 201 gctgggaggaagacagg 185

>gi|15878939|emb|AJ334521.1|HSA334521 Homo sapiens genomic sequence surrounding NotI
NL1-FH17R
Length = 748

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34

|||||||||||||||||

Sbjct: 201 gctgggaggaagacagg 185

>gi|15870433|emb|AJ326039.1|HSA326039 Homo sapiens genomic sequence surrounding NotI
NL1-DF17C
Length = 609

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34

|||||||||||||||||

Sbjct: 201 gctgggaggaagacagg 185

>gi|5579391|gb|AF161267.1|AF161267 Toxoplasma gondii catalase gene, complete cds
Length = 6957

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 24 aggaagacaggaccct 40

||||||||||||||||||

Sbjct: 6423 aggaagacaggaccct 6439

>gi|14715658|emb|AL161651.13|AL161651 Human DNA sequence from clone RP11-449I17 on c
sequence [Homo sapiens]
Length = 211627

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 23 gaggaagacaggaccct 39

||||||||||||||||||

Sbjct: 183591 gaggaagacaggaccct 183575

>gi|14041741|emb|AL133351.33|AL133351 Human DNA sequence from clone RP1-90J20 on chr
complete sequence [Homo sapiens]
Length = 167569

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 13 ggcgcagctgggaggaag 29

||||||||||||||||||

Sbjct: 118916 ggcgcagctgggaggaag 118900

>gi|10178502|emb|AL355392.7|AL355392 Human DNA sequence from clone RP5-1187J4 on chr
Contains ESTs, STSs, GSSs and two CpG islands. Contains the
gene for novel protein similar to mouse von Ebner salivary
gland protein, the gene for a novel protein similar to rat
RYF3,>
Length = 159440

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 21 gggaggaagacaggacc 37

||||||||||||||||||

Sbjct: 126470 gggaggaagacaggacc 126454

>gi|13445335|emb|AL161779.32|AL161779 Human DNA sequence from clone RP6-29D12 on chr
complete sequence [Homo sapiens]
Length = 102528

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 15 gcagctgggaggaagac 31

||||||||||||||||||

Sbjct: 16780 gcagctgggaggaagac 16764

>gi|10944277|emb|AL121753.30|HSDJ61404 Human DNA sequence from clone RP4-61404 on ch
Contains the 3' part of the MMP24 gene for matrix
metalloproteinase 24 (membrane-inserted), the ITGB4BP gene
for integrin beta 4 binding protein, a novel gene similar
to a metalloproteinase>
Length = 150481

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Minus

Query: 19 ctgggaggaagacacagga 35

||||||||||||||||||

Sbjct: 79093 ctgggaggaagacacagga 79077

>gi|13274200|emb|AL122008.28|HSJ799P18 Human DNA sequence from clone RP4-799P18 on c
complete sequence [Homo sapiens]
Length = 144407

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Plus

Query: 18 gctgggaggaagacagg 34

||||||||||||||||||

Sbjct: 28804 gctgggaggaagacagg 28820

>gi|9408716|emb|AL121980.14|HS1007G16 Human DNA sequence from clone RP5-1007G16 on c
Contains part of the gene for a novel CUB and Sushi (SCR
repeat) domain protein, a novel high-mobility group
(nonhistone chromosomal) protein 2 (HMG2) like protein
(pseudo) gene, a he>
Length = 130604

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Minus

Query: 18 gctgggaggaagacagg 34

||||||||||||||||||

Sbjct: 6431 gctgggaggaagacagg 6415

>gi|3366580|gb|AC004049.1|AC004049 Homo sapiens chromosome .4 clone B203C23 map 4q25,
Length = 173766

Score = 34.2 bits (17), Expect = 5.2

Identities = 17/17 (100%)

Strand = Plus / Plus

Query: 17 agctgggaggaagacag 33

||||||||||||||||||

Sbjct: 146187 agctgggaggaagacag 146203

>gi|7228177|emb|AL133215.16|AL133215 Human DNA sequence from clone RP11-108L7 on chr
part of the gene for a novel Insulin-like growth factor
binding type protein with Kazal-type serine protease
inhibitor domain, the gene for a novel protein similar to

rat tricarboxylat>
Length = 181086

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 19 ctgggaggaagacagga 35

||||||||||||||||||

Sbjct: 55879 ctgggaggaagacagga 55895

>gi|57236|emb|X16362.1|RNSERPG Rat SPI-2 serine protease inhibitor gene
Length = 8005

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 23 gaggaagacaggaccct 39

||||||||||||||||||

Sbjct: 4132 gaggaagacaggaccct 4148

>gi|8017427|emb|AJ289132.1|MMU289132 Mus musculus mRNA for chondroitin 4-O-sulfotran
Length = 1715

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 15 gcagctgggaggaagac 31

||||||||||||||||||

Sbjct: 1216 gcagctgggaggaagac 1232

>gi|5420383|emb|AL034384.1|HSMTM0 Human chromosome Xq28, cosmid clones 7H3, 14D7, C1
A12197, 12G8, A09100; complete sequence bases 1..217657
Length = 217657

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Plus

Query: 22 ggaggaagacaggaccc 38

||||||||||||||||||

Sbjct: 87105 ggaggaagacaggaccc 87121

>gi|1698996|gb|U78190.1|HSU78190 Human GTP cyclohydrolase I feedback regulatory prot
complete cds
Length = 4000

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 9 cgacgcgcagctggag 25

||||||||||||||||||

Sbjct: 371 cgacgcgcagctggag 355

>gi|16549752|dbj|AK055096.1|AK055096 Homo sapiens cDNA FLJ30534 fis, clone BRAWH2001
Length = 2467

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 13 ggcgagctgggaggaag 29
|||||||||||||||||
Sbjct: 355 ggcgagctgggaggaag 339

>gi|14588673|dbj|AP003492.2|AP003492 Oryza sativa genomic DNA, chromosome 1, PAC clo
Length = 158084

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 3 cgaggccgacgcgcgc 19
|||||||||||||||||
Sbjct: 144854 cgaggccgacgcgcgc 144838

>gi|14023393|dbj|AP003001.2|AP003001 Mesorhizobium loti DNA, complete genome, sectio
Length = 345783

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 3 cgaggccgacgcgcgc 19
|||||||||||||||||
Sbjct: 344778 cgaggccgacgcgcgc 344762

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences).

Posted date: Nov 14, 2001 1:05 AM

Number of letters in database: 60,694,059

Number of sequences in database: 1,020,477

Lambda K H
1.37 0.711 1.31

Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 80,132
Number of Sequences: 1021646
Number of extensions: 80132
Number of successful extensions: 25674
Number of sequences better than 10.0: 54
length of query: 40
length of database: 4,680,328,494
effective HSP length: 18
effective length of query: 22
effective length of database: 4,661,938,866
effective search space: 102562655052
effective search space used: 102562655052
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)

S1: 12 (24.3 bits)
S2: 17 (34.2 bits)

5834183-7 Sequence alignment with 09/445614

The image shows the NCBI Nucleotide search interface. At the top, there's a decorative banner with a DNA double helix and the text "SEQUENCE" and "NUCLEOTIDE". Below it is a navigation bar with links: PubMed, Nucleotide, Protein, Genome, Structure, PopSet, Taxonomy, OMIM, Books. A search bar says "Search Nucleotide for [redacted]" with "Go" and "Clear" buttons. Below the search bar are buttons for "Limits", "Preview/Index", "History", "Clipboard", and "Details". A row of buttons at the bottom includes "Display", "GenBank", "Save", "Text", and "Add to Clipboard".

1: AF129112. Homo sapiens vani...[gi:4589140]

Related Sequences, Protein, PubMed, Taxonomy,
LinkOut

LOCUS AF129112 2397 bp mRNA PRI 20-APR-1999
 DEFINITION Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA, complete cds.
 ACCESSION AF129112
 VERSION AF129112.1 GI:4589140
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2397)
 AUTHORS Caterina, M.J., Rosen, T.A., Tominaga, M., Brake, A.J. and Julius, D.
 TITLE A capsaicin-receptor homologue with a high threshold for noxious heat
 JOURNAL Nature 398 (6726), 436-441 (1999)
 MEDLINE 99215558
 REFERENCE 2 (bases 1 to 2397)
 AUTHORS Caterina, M.J., Rosen, T.A., Tominaga, M., Brake, A.J. and Julius, D.
 TITLE Direct Submission
 JOURNAL Submitted (17-FEB-1999) Cellular and Molecular Pharmacology, University of California, 513 Parnassus, San Francisco, CA 94143, USA
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BASE COUNT 494 a 701 c 686 g 516 t

ORIGIN

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Revised: October 24, 2001.

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